

09/0

OICE

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/895,840

CRF Processing Date:

 Changed a file from non-ASCII to ASCII12/26/2001
Edited by: A (STIC stat)
Verified by: A

ENTERED

 Changed the margins in cases where the sequence text was "wrapped" down to the next line. Edited a format error in the Current Application Data section, specifically: Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____ Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer. Changed the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: _____ Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file;
 page numbers throughout text; other invalid text, such as _____ Inserted mandatory headings, specifically: _____ Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____ Other:

_____Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.
31/95

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/895,840

DATE: 12/26/2001
TIME: 17:41:40

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\12262001\I895840.raw

4 <110> APPLICANT: Guenther, Catherine
 6 <120> TITLE OF INVENTION: Transgenic mice containing RORgamma gene
 7 disruptions
 9 <130> FILE REFERENCE: R-409
 11 <140> CURRENT APPLICATION NUMBER: US 09/895,840
 12 <141> CURRENT FILING DATE: 2001-06-28
 14 <150> PRIOR APPLICATION NUMBER: US 60/215,466
 15 <151> PRIOR FILING DATE: 2000-06-29
 17 <150> PRIOR APPLICATION NUMBER: US 60/221,667
 18 <151> PRIOR FILING DATE: 2000-07-27
 20 <160> NUMBER OF SEQ ID NOS: 4
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2066
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Mus musculus
 29 <220> FEATURE:
 30 <221> NAME/KEY: misc_feature
 31 <222> LOCATION: 1527
 32 <223> OTHER INFORMATION: n = A,T,C or G
 34 <400> SEQUENCE: 1
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 36 caccggacat ctcgggagct gctggctgca aagaagaccc acacctcaca aattgaagtg 120
 37 atcccttgca agatctgtgg ggacaagtca tctggatcc actacggggt tattcacctgt 180
 38 gaggggtgca agggcttctt ccgcgcgcgc cagcagtgtatgtggccta ctccctgcacg 240
 39 cgtcagcaga actgccccat tgaccgaacc agcccaacc gatgccagca ttgcgcctg 300
 40 cagaagtgcc tggctctggg catgtcccga gatgtgtca agtttggccg aatgtccaag 360
 41 aagcagaggg acagtctaca tgcagaagtgc cagaacaac tgcacacaga gcagcaacag 420
 42 gaacaagtgg ccaagactcc tccagctggg agccgcggag cagacacact tacatacact 480
 43 ttagggctct cagatggca gctaccactg ggcgcctcac ctgacacctacc cgagccctct 540
 44 gcttgtcccc ctggccctct gagagcctca ggctctggcc caccatattc caataccttg 600
 45 gccaaaacac aggtccaggg ggccctcctgc caccttgagt atagtccaga acgaggcaaa 660
 46 gctgaaggca gagacagcat ctatagcact gacggccaac ttactcttg aagatgtgga 720
 47 cttcgaaaaaggc agggaaaccac gcatcctgaa cttgggaac cagaacacagg tccagacagc 780
 48 cactgcattc ccagttctg cagtgcacca gaggtaccat atgcctctt gacagacata 840
 49 gatgtttctgg tacagaatgt ctgcaagtcc ttccgagaga catgccagct ggcactggag 900
 50 gacccctcac ggcagcgcac caacctttt tcacggagg aggtgaccag ctaccagagg 960
 51 aagtcaatgt gggagatgtg ggagcgctgt gcccaccacc tcactgagc cattcagtat 1020
 52 gtgggtggagt ttgccaaagcg gctttcaggg ttcatggagc tctggcagaa tgaccagatc 1080
 53 atactactga cagcaggagc aatggaaagtc gtcctagtca gaatgtgcag ggcctacaat 1140
 54 gccaacaacc acacagtctt tttgaaggc aaatacggtg gtgtggagct gtttcgagcc 1200
 55 ttgggctgca gcgagctcat cagctccata tttgacttt cccacttctt cagcgccctg 1260
 56 tgggtttctg aggatgagat tgcctctac acggccctgg ttctcatcaa tgccaaaccgt 1320
 57 cctgggtctcc aagagaagag gagatggaa catctgcaat acaatttggaa actgcttcc 1380
 58 catcatcatc tctgcaagac tcatcgacaa ggcctccat ccaagctgcc acccaaagg 1440
 59 aaactccgga gcctgtgcag ccaacatgtg gaaaagctgc agatcttcca gcacccac 1500
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61 gaatccctg aggggctgtc aaagtgtatct ggaggaagga caactttcta tttccttcag 1620
 62 ccctctgacc cgtctccctg gactcccttc acccagcctt tccctttctg cactctatga 1680
 63 agggtgttat cccttaggat aagcaaattcc taagactgtat ttctgtcccc taggcttgcc 1740
 64 ttgttagaca acagcacaa gtatggaga aaaggctgt tatgtttgtat ttcccataag 1800
 65 ttccaccctg gtttctggaa gctgtgggtt agatggata gagataggat gaccaagtca 1860
 66 aataaaaaaac agactgacaa tcagcaggga taaatccagg tacctggat aaggagaact 1920
 67 caaatctagg cttgaaagct aataacagtc cttcaatac ctcattgtat ttcccatgg 1980
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 69 gtatataata agaatataga ttccctg 2066
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 72 <211> LENGTH: 516
 73 <212> TYPE: PRT
 74 <213> ORGANISM: Mus musculus
 76 <400> SEQUENCE: 2
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 78 1 5 10 15
 79 Ala Ala Lys Lys Thr His Thr Ser Gln Ile Glu Val Ile Pro Cys Lys
 80 20 25 30
 81 Ile Cys Gly Asp Lys Ser Ser Gly Ile His Tyr Gly Val Ile Thr Cys
 82 35 40 45
 83 Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Gln Gln Cys Asn Val Ala
 84 50 55 60
 85 Tyr Ser Cys Thr Arg Gln Gln Asn Cys Pro Ile Asp Arg Thr Ser Arg
 86 65 70 75 80
 87 Asn Arg Cys Gln His Cys Arg Leu Gln Lys Cys Leu Ala Leu Gly Met
 88 85 90 95
 89 Ser Arg Asp Ala Val Lys Phe Gly Arg Met Ser Lys Lys Gln Arg Asp
 90 100 105 110
 91 Ser Leu His Ala Glu Val Gln Lys Gln Leu Gln Gln Gln Gln Gln
 92 115 120 125
 93 Glu Gln Val Ala Lys Thr Pro Pro Ala Gly Ser Arg Gly Ala Asp Thr
 94 130 135 140
 95 Leu Thr Tyr Thr Leu Gly Leu Ser Asp Gly Gln Leu Pro Leu Gly Ala
 96 145 150 155 160
 97 Ser Pro Asp Leu Pro Glu Ala Ser Ala Cys Pro Pro Gly Leu Leu Arg
 98 165 170 175
 99 Ala Ser Gly Ser Gly Pro Pro Tyr Ser Asn Thr Leu Ala Lys Thr Glu
 100 180 185 190
 101 Val Gln Gly Ala Ser Cys His Leu Glu Tyr Ser Pro Glu Arg Gly Lys
 102 195 200 205
 103 Ala Glu Gly Arg Asp Ser Ile Tyr Ser Thr Asp Gly Gln Leu Thr Leu
 104 210 215 220
 105 Gly Arg Cys Gly Leu Arg Phe Glu Glu Thr Arg His Pro Glu Leu Gly
 106 225 230 235 240
 107 Glu Pro Glu Gln Gly Pro Asp Ser His Cys Ile Pro Ser Phe Cys Ser
 108 245 250 255
 109 Ala Pro Glu Val Pro Tyr Ala Ser Leu Thr Asp Ile Glu Tyr Leu Val
 110 260 265 270
 111 Gln Asn Val Cys Lys Ser Phe Arg Glu Thr Cys Gln Leu Arg Leu Glu

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112	275	280	285
113	Asp Leu Leu Arg Gln Arg Thr Asn Leu Phe Ser Arg Glu Glu Val Thr		
114	290	295	300
115	Ser Tyr Gln Arg Lys Ser Met Trp Glu Met Trp Glu Arg Cys Ala His		
116	305	310	315
			320
117	His Leu Thr Glu Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Leu		
118	325	330	335
119	Ser Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Ile Leu Leu Thr		
120	340	345	350
121	Ala Gly Ala Met Glu Val Val Leu Val Arg Met Cys Arg Ala Tyr Asn		
122	355	360	365
123	Ala Asn Asn His Thr Val Phe Phe Glu Gly Lys Tyr Gly Gly Val Glu		
124	370	375	380
125	Leu Phe Arg Ala Leu Gly Cys Ser Glu Leu Ile Ser Ser Ile Phe Asp		
126	385	390	395
			400
127	Phe Ser His Phe Leu Ser Ala Leu Cys Phe Ser Glu Asp Glu Ile Ala		
128	405	410	415
129	Leu Tyr Thr Ala Leu Val Leu Ile Asn Ala Asn Arg Pro Gly Leu Gln		
130	420	425	430
131	Glu Lys Arg Arg Val Glu His Leu Gln Tyr Asn Leu Glu Leu Ala Phe		
132	435	440	445
133	His His His Leu Cys Lys Thr His Arg Gln Gly Leu Leu Ala Lys Leu		
134	450	455	460
135	Pro Pro Lys Gly Lys Leu Arg Ser Leu Cys Ser Gln His Val Glu Lys		
136	465	470	475
			480
137	Leu Gln Ile Phe Gln His Leu His Pro Ile Val Val Gln Ala Ala Phe		
138	485	490	495
139	Pro Pro Leu Tyr Lys Glu Leu Phe Ser Thr Asp Val Glu Ser Pro Glu		
140	500	505	510
141	Gly Leu Ser Lys		
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145	<210> SEQ ID NO: 3		
146	<211> LENGTH: 200		
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151	<223> OTHER INFORMATION: Targeting vector		
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155	gagaccagtg cacatgaatt ggaggtccct gggaccacct caaactccga gagggtgaaa	120	
156	taagcagtt ctgtttcca gggcttcttc cgccgcagcc agcagtgtaa tgtggcctac	180	
157	tcctgcacgc gtcagcagaa	200	
159	<210> SEQ ID NO: 4		
160	<211> LENGTH: 200		
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164	<220> FEATURE:		
165	<223> OTHER INFORMATION: Targeting vector		
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168 catacacttt agggctctca gatgggcagc taccactggg cgccctcacct gacctacccg 60
169 aggccctctgc ttgtccccct ggccctcctga gagcctcagg ctctggccca ccatattcca 120
170 ataccttggc caaaacagag gtccaggggg cctcctgcca ctttgagttt agtccagaac 180
171 gaggcaaagc tgaaggcaga 200

VERIFICATION SUMMARY

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L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1